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OM protein - protein search, using sw model

Run on: May 8, 2002, 11:08:00 ; Search time 28.8 Seconds
 (without alignments)
 2701.975 Million cell updates/sec

Title: US-09-911-513-2

Perfect score: 2758

Sequence: 1 MKRDHHHHQDKKTMNNEE.....MLGWHTRPLIATSAWKLSTN 532

Scoring table: BL050M62

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_17:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query	Match	Length	DB	ID	Description
1	2758	100.0	532	10	O23724		O23724 arabidopsis
2	2754	99.9	532	10	O23643		O23643 arabidopsis
3	2747.5	99.6	533	10	O91qt8		O91qt8 arabidopsis
4	2189.5	79.4	587	10	O9SLH3		O9SLH3 arabidopsis
5	2185.5	79.2	587	10	O23725		O23725 arabidopsis
6	2179.5	79.0	587	10	O9STF48		O9STF48 zea mays (m)
7	1602.5	58.1	630	10	O9MB96		O9MB96 oryza sativ
8	1595.5	57.8	625	10	O9STP59		O9STP59 triticum ae
9	1594	57.8	623	10	O9AYK4		O9AYK4 pism sativ
10	1587	57.5	511	10	O9CBY3		O9CBY3 arabidopsis
11	1581	57.3	662	10	O63367		O63367 arabidopsis
12	1552.5	56.3	547	10	O9SRP9		O9SRP9 arabidopsis
13	1490	54.0	523	10	O9Lf53		O9Lf53 arabidopsis
14	967.5	35.0	493	10	O9AS97		O9AS97 oryza sativ
15	608.5	22.1	819	10	O9AVK4		O9AVK4 pism sativ
16	602.5	21.8	653	10	O9A384		O9A384 arabidopsis
17	598.5	21.7	653	10	O9E304		O9E304 arabidopsis
18	590.5	21.4	490	10	O9DDL7		O9DDL7 arabidopsis
19	590.5	21.4	668	10	O9FUZ7		O9FUZ7 zea mays (m)

ALIGNMENTS

RESULT	1
023724	PRELIMINARY;
ID	023724;
AC	O23724;
DT	01-JAN-1998 (TREMBL) 05, Created)
37	440 16.0 1336 10 081074 arabidopsis
38	431 15.6 284 10 09X557 arabidopsis
39	429 15.6 375 10 09LNX6 arabidopsis
40	428 15.5 583 10 09SNB8 arabidopsis
41	422.5 15.3 542 10 09SCRO arabidopsis
42	418.5 15.2 287 10 09M055 arabidopsis
43	412 14.9 325 10 09X52 arabidopsis
44	407 14.8 718 10 080933 arabidopsis
45	393.5 14.3 531 10 09SZF7 arabidopsis

RP	SEQUENCE FROM N.A.
RC	STRAIN=LANDSBERG ERECTA;
RX	MEDLINE=98051192; PubMed=9389651;
RA	Peng J., Carol P., Richards D.E., King K.E., Cowling R.J., Murphy G.P., Harberd N.P.;
RA	RT regulates gibberellin responses. ";
RA	The Arabidopsis GAI gene defines a signaling pathway that negatively
[1]	regulates gibberellin responses. ";
RN	[1]
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RX	MEDLINE=98051192; PubMed=9389651;
RA	Peng J., Carol P., Richards D.E., King K.E., Cowling R.J., Murphy G.P., Harberd N.P.;
RA	RT regulates gibberellin responses. ";
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RL	RT regulates gibberellin responses. ";
DR	DR Mendel: 24070; Arath: 13051-24070.
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RT	RT regulates gibberellin responses. ";
RL	RL Genes Dev: 11:

Qy	60	QEDDSQSLATEVHVNPAELYTWLDSMLTDLNPPSSNAEYDLKALPGDALLNQFADSDAS	119
Db	61	QEDDSQSLATEVHVNPAELYTWLDSMLTDLNPPSSNAEYDLKALPGDALLNQFADSDAS	120
Qy	120	SSNQGGGDDTTNNKLCKCSNGVVETTATAESTRHVLVLDQEQNGVRVLYHALLACEAV	179
Db	121	SSNQGGGDDTTNNKLCKCSNGVVETTATAESTRHVLVLDQEQNGVRVLYHALLACEAV	180
Qy	180	QKENLTVAELVKQIGFLAYSQIGMRKVATYFAEALARRIYRLSPSQSPIDHSLSDTLQ	239
Db.	181	QKENLTVAELVKQIGFLAYSQIGMRKVATYFAEALARRIYRLSPSQSPIDHSLSDTLQ	240
Qy	240	MHFYETCPYLKFKAHTFTANQAILEAFQGKRVHVIDFMSQGLWPALMOALRPGGPPV	299
Db.	241	MHFYETCPYLKFKAHTFTANQAILEAFQGKRVHVIDFMSQGLWPALMOALRPGGPPV	300
Qy	300	FRLTGIGPPADDNFYTLHEVGCKLHLAAEAHVVEFYRGEVANTIA LDADSMLELRPSEI	359
Db.	301	FRLTGIGPPADDNFYTLHEVGCKLHLAAEAHVVEFYRGEVANTIA LDADSMLELRPSEI	360
Qy	360	ESAVAVNSVFEHLKLGRPGAIDKVGVNVNIKEPEFTVVEQESNNINSPIFLDRTELSLY	419
Db.	361	ESAVAVNSVFEHLKLGRPGAIDKVGVNVNIKEPEFTVVEQESNNINSPIFLDRTELSLY	420
Qy	420	YSTLFDSLEGYPSCQDKVMSEVYLGKQICNVACGPDRVERHETLSQWRNRFGSAGFAA	479
Db.	421	YSTLFDSLEGYPSCQDKVMSEVYLGKQICNVACGPDRVERHETLSQWRNRFGSAGFAA	480
Qy	480	AHIGSNFAKQASMLIALFNGEGYRVEEEDGCLMLGWHTRPLIAWSWKLSTN	532
Db.	481	AHIGSNFAKQASMLIALFNGEGYRVEEEDGCLMLGWHTRPLIAWSWKLSTN	533

Db	121	PVLPSPEICGFPASDYLKVPGNAAYQFPADSSSSN	172	-----QNKEKLKSCSPD
Qy	141	-----GVV-----ETTATAESTRHVLYDSEQNGYRLVHALLACAEAV	179	
Db	173	SMVTSTSTGTQIGGVTTTTTAESTRSVLYDSEQNGYRLVHALLACAEAI	232	
Qy	180	QKENLTVAEALVKQIGFLAVSOIGAMEKVTYFAEALARRYPLSPSQSPTDHSLSDTLQ	239	
Db	233	QNNNTTAAEALVKQIGCLAVSOAGAERKVTYFAEALARRYPLSPQNQIDHCLSDTLQ	292	
Qy	240	MHFYETCPYKLFAHTANQAILEAFQGKKRVHVIDFMSQGQLQWPALMQALRPGGPPV	299	
Db	293	MHFYETCPYKLFAHTANQAILEAFQGKKRVHVIDFMMNGQLMQALRREGGPP	352	
Qy	300	FRLTGIGPPADDNFVDIHEYCKLAKHLAEEA1HVEEFYERGFYANTLADASMLELRSEI	359	
Db	353	FRLTGIGPPADDNSDHLEYCKLAKLAEEA1HVEEFYERGFYANSLADASMLELRSEI	412	
Qy	360	ESVAVNSVFEIHLKLGRPGALDKVLGVNVNQIKPTEIVVQEQQSNHNSPIFLDRFTESLYH	419	
Db	413	ESVAVNSVFEIHLKLGRPGGLEKVLGVVKQIKPVIFTIVQEQQSNHNGPVFLDRFTESLYH	472	
Qy	420	YSTLEDSLEGYPGQSKVMSMVEWYLGKQICQNYVACGDPRVERHETLSQWRNRFGQSAGFAA	479	
Db	473	YSTLEDSLEGYPNSQDRKVMSEVYLGKQICQNYVACEGDRVERHETLSQWRNRFGSSGLAP	532	
Qy	480	AHTGSNAFKQPSMMLALEFGEGYRYEESDGCLMLGHTRPLATSAWKLT	531	
Db	533	AHGSNAFKQPSMMLSVNSQGYREEVNGMLGHTRPLITSAWKLT	584	
RESULT	5			
Q9SLH3		PRELIMINARY;	PRT;	587 AA.
ID				
AC	Q9SLH3_			
DT	01-MAY-2000	(TREMBLrel.	13, Created)	
DT	01-MAY-2000	(TREMBLrel.	13, Last sequence update)	
DT	01-MAY-2000	(TREMBLrel.	13, Last annotation update)	
DE	PUTATIVE_RGA1	GIBBERELLIN RESPONSE MODULATION PROTEIN.		
GN	AT2G01570			
OS	Oryza sativa	(Mouse-ear cress);		
OC	Bukaryota; Viridiplantae; Streptophytina; Embryophyta;			
OC	Spermatophytina; Magnoliophytina; eudicots; Rosidae;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP		SEQUENCE FROM N.A.		
RC		STRAIN=CV COLUMBIA;		
RX		MEDLINE=20083487; PubMed=10617197;		
RA	Xanl, S.,	Roussley, S.D., Shea, T.P., Benito, M.-I., Town, C.D.,		
RA	Fujii, C.Y., Mason, T.M., Bowman, C.L., Barnstead, M.E., Feldblum, T.V.,			
RA	Buell, C.R., Ketchum, K.A., Lee, J.J., Ronning, C.M., Koo, H., Moffat, K.S.,			
RA	Cronin, L.A., Shen, M., Vanek, S.E., Umayam, L., Tallon, L.J., Gill, J.E.,			
RA	Adams, M.D., Carrera, A.J.H., Creasy, T.H., Goodman, H.M., Nieman, W.C., Eisen, J.A.,			
RA	Copenhaver, G.P., Preuss, D., Salzberg, S.L., Fraser, C.M., Venter, J.C.,			
RA	"Sequence and analysis of chromosome II of <i>Arabidopsis thaliana</i> ."			
RL	Nature 402:761-768 (1999).			
DR	EMBL; AC005560; AAC053341.			
SO	SEQUENCE	587 AA;	64035 MW;	

Db	61	EVALKLEQLETTMMSNQEDGLSHIATDTHVNPESELWSLDNLSELNPPLPASSNGLD	120		Db	121	PVLPSPEICGFPASDYDLEVIPGNAYQFPAIDSSSSN-----NONKRKLCSSPD	172	
Oy	97	-----AEYDLKAIPGDAILNQFAIDSASSSNQGGDTTYTNKRLK-CSN-----	140		Oy	141	-----GVV-----ETTATAESTRHYLVDSOENGVRLYHALLACEAV	179	
Db	121	PVLPSPEICGFPASDYDLKTPGNAYQFPAIDSSSSN-----NONKRKLCSSPD	172		Db	173	SMVTSTSTGTQIGGYIGTVTTTAAESTRVSLLVDSQENGVRVLYHALLACEA	232	
Oy	141	-----GVY-----ETTATAESTRHYLVDSOENGVRLYHALLACEAV	179		Qy	180	QKENUTVAELVKQIGFLAYSQIGAMRKVATYFAEALARRIYSLSPSQSPIDHSLSDTLQ	239	
Db	173	SMVTSTSTGTQIGGYIGTVTTTAAESTRVSLLVDSQENGVRVLYHALLACEA	232		Db	233	QNNNTLAELVKQIGFLAYSQIGAMRKVATYFAEALARRIYSLSPSQSPIDHSLSDTLQ	292	
Oy	180	QKENUTVAELVKQIGFLAYSQIGAMRKVATYFAEALARRIYSLSPSQSPIDHSLSDTLQ	239		Oy	240	MHFYETCPYLKFAHTANQAILEAQGKKRVAIDFSMSQGLONPALMQLALRPGGPPV	299	
Db	233	QNNNTLAELVKQIGFLAYSQIGAMRKVATYFAEALARRIYSLSPSQSPIDHSLSDTLQ	292		Db	293	MHFYETCPYLKFAHTANQAILEAQGKKRVAIDFSMSQGLONPALMQLALRPGGPPV	352	
Oy	240	MHFYETCPYLKFAHTANQAILEAQGKKRVAIDFSMSQGLONPALMQLALRPGGPPV	299		Qy	300	FRLTGIGPAPDNFDLYHEVGCKLAHLAAEAIAHVEFYEYRFVANTLADLDSMLERLPSEI	359	
Db	293	MHFYETCPYLKFAHTANQAILEAQGKKRVAIDFSMSQGLONPALMQLALRPGGPPV	352		Db	353	FRLTGIGPAPDNFDLYHEVGCKLAHLAAEAIAHVEFYEYRFVANTLADLDSMLERLPSEI	412	
Oy	300	FRLTGIGPAPDNFDLYHEVGCKLAHLAAEAIAHVEFYEYRFVANTLADLDSMLERLPSEI	359		Qy	360	ESAVNSYFELHKLKGPKAIDKTYLGVYVNOIKPEIIFTVQEESNHNSPIFLDRTESTHY	419	
Db	353	FRLTGIGPAPDNFDLYHEVGCKLAHLAAEAIAHVEFYEYRFVANTLADLDSMLERLPSEI	412		Db	413	ESAVNSYFELHKLKGPKAIDKTYLGVYVNOIKPEIIFTVQEESNHNSPIFLDRTESTHY	472	
Oy	360	ESAVNSYFELHKLKGPKAIDKTYLGVYVNOIKPEIIFTVQEESNHNSPIFLDRTESTHY	419		Qy	420	YSTLFDSLQEVPSGDKVMSEVYLGKQICNVAQCDPDRVERHETLSQWRNRFGSAGFAA	479	
Db	413	ESAVNSYFELHKLKGPKAIDKTYLGVYVNOIKPEIIFTVQEESNHNSPIFLDRTESTHY	472		Db	473	YSTLFDSLQEVPSGDKVMSEVYLGKQICNVAQCDPDRVERHETLSQWRNRFGSAGFAA	532	
Oy	420	YSTLFDSLQEVPSGDKVMSEVYLGKQICNVAQCDPDRVERHETLSQWRNRFGSAGFAA	479		Qy	480	AHGSNAFKQASMLIALFNGGEGYRVEEDGCLMLGWHTRPLITSAWKLST	531	
Db	473	YSTLFDSLQEVPSGDKVMSEVYLGKQICNVAQCDPDRVERHETLSQWRNRFGSAGFAA	532		Db	533	AHGSNAFKQASMLIALFNGGEGYRVEEDGCLMLGWHTRPLITSAWKLST	584	
Oy	480	AHGSNAFKQASMLIALFNGGEGYRVEEDGCLMLGWHTRPLITSAWKLST	531		RESULT	7			
Db	533	AHGSNAFKQASMLIALFNGGEGYRVEEDGCLMLGWHTRPLITSAWKLST	584		Q9ST48	PRELIMINARY;	PRT;	630 AA.	
RESULT	6				Q9ST48	PRELIMINARY;	PRT;	630 AA.	
ID	023725				AC	09ST48;			
AC	023725	PRELIMINARY;	PRT;	587 AA.	DT	01-MAY-2000	(TREMBLrel.	13, Created)	
DT	01-JAN-1998	(TREMBLrel.	05, Created)		DT	01-MAY-2000	(TREMBLrel.	13, Last sequence update)	
DT	01-JAN-1998	(TREMBLrel.	05, Last sequence update)		DT	01-MAR-2001	(TREMBLrel.	16, Last annotation update)	
DE	GRS PROTEIN				DE	DE	GIBBERELLIN RESPONSE MODULATOR (FRAGMENT).		
OS	Arabidopsis thaliana (Mouse-ear cress).				D8	OS	Zea mays (Maize).		
CC	Eukaryota; Viridiplantes; Streptophytina; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Magnoliopsida; Liliopsida; Poaceae; PACC clade; OC				RA	OC	Bukaryote; Viridiplantes; Streptophytina; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Magnoliopsida; Liliopsida; Poaceae; PACC clade; OC		
CC	eurosts II; Brassicaceae; Rosidae; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; OC				RA	RA	Panicoidae; Andropogoneae; Zea; NCBI_TaxID=4577;		
FN	[1]				RN	RN	SEQUENCE FROM N.A.		
FN	NCBI_TaxID=3702;				RX	RX	MEDLINE=93347734; PubMed=10421366;		
RP					RA	Peng J., Richards D.E., Hartley N.M., Murphy G.P., Devos K.M., Flintham J.E., Beales J., Fish L.J., Worland A.J., Pelica F., Sudhakar D., Christou P., Shape J.W., Gale M.D., Harberd N.P.; RT			
SEQUENCE FROM N.A.					RA	"Green revolution" genes encode mutant gibberellin response modulators." RL	Nature 400:256-261(1999).		
STRAIN=COLUMBIA;					RT	DR	EMBL: AJ242530, CAB1557.1; -.		
RA	Peng J., Carol P., Richards D.E., King K.E., Cowling R.J., Murphy G.P., Harberd N.P.; RT				FT	NON_TER	630		
RA	Genes Dev. 0:0(0)				SQ	SEQUENCE	630 AA; 66028 MW; 3D56851726cc51042 CRC64;		
RL	Y15194; CAA75493.1; -								
DR	Mendl; 24071; Arath; 3051; 24071.								
SEQUENCE	587 AA; 64006 MW; F6FC7738EE7DCA9 CRC64;								
Query Match	79.0%	Score 2179.5; DB 10; Length 587;			Query Match	58.1%	Score 1602.5; DB 10; Length 630;		
Best Local Similarity	74.0%	Pred. No. 3e-159; Mismatches 41; Indels 69; Gaps 9;			Best Local Similarity	54.0%	Pred. No. 8.1e-115; Mismatches 68; Indels 119; Gaps 15;		
Matches	438; Conservative				Matches	34; Conservative			
Oy	1	MKRDHHH----HH-----QDKTMAMNEEDDGNGM-DLLAVGYKVRSEMA 43			Oy	1	MKRDHHHHD-----KKTMAMNEEDDGNGM-DLLAVGYKVRSEMA 42		
Db	1	MKRDHQFOGRLLSNGTSSSSISKDNNMVKKEEDGGNMDDLLAVGYKVRSEMA 60			Db	1	MKRE---YQDAGGSGDMGSSKDKMMAAAAGAGEQQED--VDELAAALGYKVRSEMA 53		
Oy	44	DVAQKLEQLEMMMSNQEDDSQSLATEVHYNPABLYWLDSMILTDLNPP---SSN---	96		Qy	43	ADVAQKLEQLEVM-----SNQEDD-L-SQSLATEVHYNPABLYWLDSMILTDLNPP 93		
Db	61	EVALKLEQLETTMMSNQEDGLSHIATDTHVNPESELWSLDNLSELNPPLPASSNGLD 120			Db	54	ADVAQKLEQLEMMMSNQEGLSHLAAADTYHNPABLYWLDSMILTDLNPP 113		
Oy	97	-----AEYDLKAIPGDAILNQFAIDSASSSNQGGGGDTTYTNKRLK-CSN-----	140		Qy	94	-----SSNAEYDLKAIPGDAILNQFAIDSASSSNQGGGGDTTYTNKRLK-CSN-----	115	

Qy 220 ----IVRLSP--SQSPIDHSLSDTLOMHFETCPVLFKAFTANQAILAEFQKKRKHV 272
 Db 501 SSCLGIYATLPYSHTHNOKVASAFQV-FENGISPVKESEHTANGAIEAFEREERHV 559
 Qy 273 IDFSMSGQLQWPALMOMALLRPGPPVERLIGIGPAPDNPFDYLHVGCKLAHLABAHV 332
 Db 560 IDLDIMQGLQWGLFLHTLASRPGGPPYVRGLG---TSMETLEATGKRLSDFANKLGL 615
 Qy 333 PEPEYRGF-VANTILADDASMLPLRPSITESAVNSYELIKLGRGAIDKVLGVVNQIK 391
 Db 616 PPEF--PPVAEKVGNDIVEKLNV--SKSEAVAH--WLQHSLYDVTGSDINTLWLQRLA 669
 Qy 392 PEIIFTVVQESENHNNSPISPLFLDRFTESELHYSTLFDSU--EGVPSGDVKMSEVYLGKQIC 448
 Db 670 PKVVTVEQDLN-NAASFGLGREAVATHYSAIFDSLGSSTGEESERHVVYEQQLLSREIR 728
 Qy 449 NVVACDGPR--VERHETLSOWRNREGSAGFAAAHIGSNAFKOQSMILLALEFNGGYRV 505
 Db 729 NYLAVGSPRSGEIKEFH---NWREKLQQCSFRGVSLAGNARATQSLLGMF-PSEGYTL 783
 Qy 506 ERSDGCMUMLGNWTRPLIASWK 528
 Db 784 VEDNGILKLGWKDCLLTASAWR 806

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